

Multi-Environment Assessment of Climate-Resilient *Oryza sativa* L. Genotypes through Genotype $\times$ Environment Interaction Analysis and AMMI Modeling

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Received: 05 Dec 2024

Revised: 23 Dec 2024

Accepted: 04 Jan 2025

Published: 27 Jan 2025

E-ISSN: 2989-5340

DOI: <https://doi.org/10.54660/jafi.2025.5.1.11-19>

ABSTRACT

Background: The production of rice (*Oryza sativa* L.) is being affected increasingly by climate variability, such as heat stress, drought, flooding, and salinity. The interaction of genotype and environment (G $\times$ E) makes it hard to identify stable high-yield genotypes hence the importance of G $\times$ E.

Objectives: The study evaluated the extent of G $\times$ E interaction among rice genotypes and identified genotypes that were high-yielding, stable and widely adapted using AMMI analysis.

Materials and Methods: Twenty rice genotypes were evaluated in six contrasting environments representing irrigated, drought, flood, saline and heat-stress conditions in a Randomized Complete Block Design with three replications. Combined ANOVA, AMMI model, AMMI Stability Value (ASV) and Yield Stability Index (YSI) were used to analyze grain yield and grain yield-related agronomic traits.

Results: The largest percentage of the variation in yield was contributed by environmental effects followed by G $\times$ E interaction and genotype effects. Most of the interaction variation was explained by the first two interaction principal components. The genotypes CR-Dhan801, CR-Dhan805 and CR-Dhan812 exhibited high yield performance with low stability values, indicating broad adaptation while the other genotypes showed environment specific adaptation.

Conclusion: AMMI analysis proved effective in identifying stable and adaptable rice genotypes and can provide valuable support for climate resilient breeding programs. Among them, stable genotypes can be prioritized for cultivation and can be used as promising parents for developing stress-tolerant varieties of rice.

Keywords: climate-resilient rice, genotype $\times$ environment interaction, AMMI analysis, multi-environment trial, yield stability, stress adaptation, quantitative genetics

1. Introduction

1.1. Global Importance of Rice and the Challenge of Climate Variability

Oryza sativa L. has developed into the staple food for more than half of the world population and is essential for food safety and support of livelihoods of enormous numbers of smallholders in Asia, Africa, and Latin America (Khush, 2005) ^[1]. Worldwide, rice production operates under a variety of conditions such as irrigated lowlands, rainfed lowlands, rainfed uplands, and deep-water ecosystems, which vary in terms of climates and other hydrological aspects (Mohanty *et al.*, 2013; Wassmann *et al.*, 2009) ^[2, 3]. The effects of climate changes have influenced the incidence of abiotic stresses responsible for destabilizing rice growing systems (Wassmann *et al.*, 2009; Zhao *et al.*, 2017) ^[3, 4].

1.2. Heat, Drought, Flooding, and Salinity Stress in Rice

High heat stress of over 33-35 degrees Celsius during the flowering stage has a negative effect on the fertility of spikelets due to its impact on the viability of pollen and anther dehiscence while constant drought during the vegetative and reproductive phase leads to the limitation of tillering, emergence of panicles and filling of the grains (Jagadish *et al.*, 2007; Kumar *et al.*, 2014) ^[6, 12]. Heavy flooding and prolonged submersion eliminate oxygen and light leading to depletion of carbohydrates and shoot elongation in preparation of recovery after the stress. Salinity causes osmotic and ionic stress leading to reduction of photosynthetic efficiency and loss of ion homeostasis (Ismail & Horie, 2017) ^[7]. Different stresses present different physiological mechanisms making it impossible to find one genotype that will be resistant in all environments of the stress type, hence the necessity of conducting multi-environment testing when selecting crops for planting in regions affected by climate change factors.

1.3. Climate-Resilient Rice Genotypes and Breeding Approaches

The notion of climate resilience in rice breeding can be summarily described as the capability of a genotype to achieve economically viable yield and quality even in the presence of negative effects on the growth that occur due to external events or situations (Atlin *et al.*, 2017) ^[8]. The implementation of genetic variability for breeding is based on the use of traditional varieties of rice,

species that are distantly related and those that have been bred specifically to be resistant to a negative effect (Collard & Mackill, 2008; Crossa *et al.*, 2017) ^[9,10]. The use of interspecific hybridization has made it possible to introduce into the known gene pool of traditional varieties genetic factors, like SUB1 that provides for the rice ability to grow under submerged conditions, as well as on-drought yield-causing genes, such as the series of genes that make up qDTY set of rice varieties (Xu *et al.*, 2006) ^[11].

1.4. Genotype × Environment Interaction and the Rationale for Multi-Environment Testing

Genotype – environment interaction (G×E) means that the same genotype may respond differently to the environmental conditions, causing it to have a different relative performance in different environments. G×E results from the differences in the way genotypes respond to changes in the environment (crossover interaction) and also the differences related to scaling of the responses in the environment (non-crossover interaction). Due to the presence of crossover interactions, the results obtained from single site trials are not reliable. This is because crossover interactions influence the ranking of genotype performance. In this context, it is crucial to conduct multi-environment trials (MET) that involve an effective interaction analysis so that reliable genotypes can be identified.

1.5. Objectives of the Study

The current study aims to achieve a number of objectives, which include: (i) performance assessment of twenty rice varieties for concerning agronomic field operations, physiological traits and yield in six different climatic conditions; (ii) use of a combination of variance analysis to assess partitioning of phenotypic variation into genotypic, environmental and G by E components; (iii) utilization of AMMI modeling for revealing G×E interaction structure and doing calculations of stability parameters such as ASV and YSI; and (iv) determination of rice varieties that are more adaptable to different climatic conditions.

2. Materials and Methods

2.1. Plant Material

Twenty rice genotypes were assembled for evaluation, comprising 17 advanced breeding lines developed for tolerance to submergence, drought, salinity, or heat stress, together with three widely grown check cultivars representing irrigated, rainfed lowland, and broadly adapted production systems (Table 1). Genotypes were selected to represent contrasting pedigree backgrounds, including crosses derived from stress-tolerance donor sources and locally adapted recurrent parents, so as to capture a representative range of genetic variability for climate resilience traits.

Table 1: Rice genotypes evaluated in the multi-environment trial, including pedigree background, maturity group, and principal adaptive characteristic.

Code	Genotype	Pedigree / Source	Maturity Group	Principal Adaptive Trait
G1	CR-Dhan801	IR64 / Sub1 donor	Medium (120-125 d)	Submergence tolerance (SUB1 QTL)
G2	CR-Dhan802	Swarna / drought donor line	Medium (118-123 d)	Reproductive-stage drought tolerance
G3	CR-Dhan803	Pokkali / elite lowland line	Medium-Late (128-132 d)	Salinity tolerance (Saltol)
G4	CR-Dhan804	N22 / heat-tolerant donor	Early (105-110 d)	Spikelet fertility under heat stress
G5	CR-Dhan805	Multi-parent stress-tolerant composite	Medium (122-127 d)	Combined drought-submergence tolerance
G6	CR-Dhan806	IR64-Sub1 / drought QTL line	Medium (120-124 d)	Submergence + drought tolerance
G7	CR-Dhan807	Local landrace / IR64	Late (130-135 d)	Deep root system, terminal drought
G8	CR-Dhan808	Saltol donor / high-yield line	Medium (124-128 d)	Salinity tolerance, seedling stage
G9	CR-Dhan809	N22 / Swarna	Early (108-112 d)	Heat escape via early flowering
G10	CR-Dhan810	qDTY donor composite	Medium (119-123 d)	Yield under vegetative-stage drought
G11	CR-Dhan811	Sub1 / Saltol combined donor	Medium (121-126 d)	Submergence and salinity tolerance
G12	CR-Dhan812	Elite recurrent parent / stress composite	Medium (120-125 d)	Broad multi-stress tolerance
G13	CR-Dhan813	Landrace-derived, drought donor	Late (129-134 d)	Osmotic adjustment under drought
G14	CR-Dhan814	Heat donor / lowland elite line	Early-Medium (112-118 d)	Pollen viability under heat stress
G15	CR-Dhan815	Saltol / Pokkali derivative	Medium-Late (126-131 d)	Reproductive-stage salinity tolerance
G16	CR-Dhan816	Multi-donor pyramided line	Medium (121-126 d)	Combined heat-drought tolerance
G17	CR-Dhan817	Sub1 introgression, elite background	Medium (118-122 d)	Rapid post-submergence recovery
G18 (Check)	IR64	Standard check, broadly adapted	Medium (120-125 d)	Wide adaptation, moderate stress tolerance
G19 (Check)	Swarna	Standard rainfed lowland check	Medium-Late (128-132 d)	Rainfed lowland adaptation
G20 (Check)	BRRI dhan28	Standard irrigated check	Early-Medium (115-120 d)	High-input irrigated performance

2.2. Experimental Locations and Environmental Characterization

Field trials were conducted across six locations selected to represent the principal rice production ecologies exposed to climate-related stress: irrigated lowland (E1), rainfed upland (E2), drought-prone lowland (E3), flood/submergence-prone lowland (E4), saline coastal lowland (E5), and a heat-stress-

prone irrigated site (E6) (Table 2, Figure 1). Environmental characterization included seasonal rainfall distribution, mean and maximum temperature during the reproductive window, soil texture and electrical conductivity, and duration and depth of flooding where relevant, enabling each site to be treated as a distinct testing environment in the combined analysis.

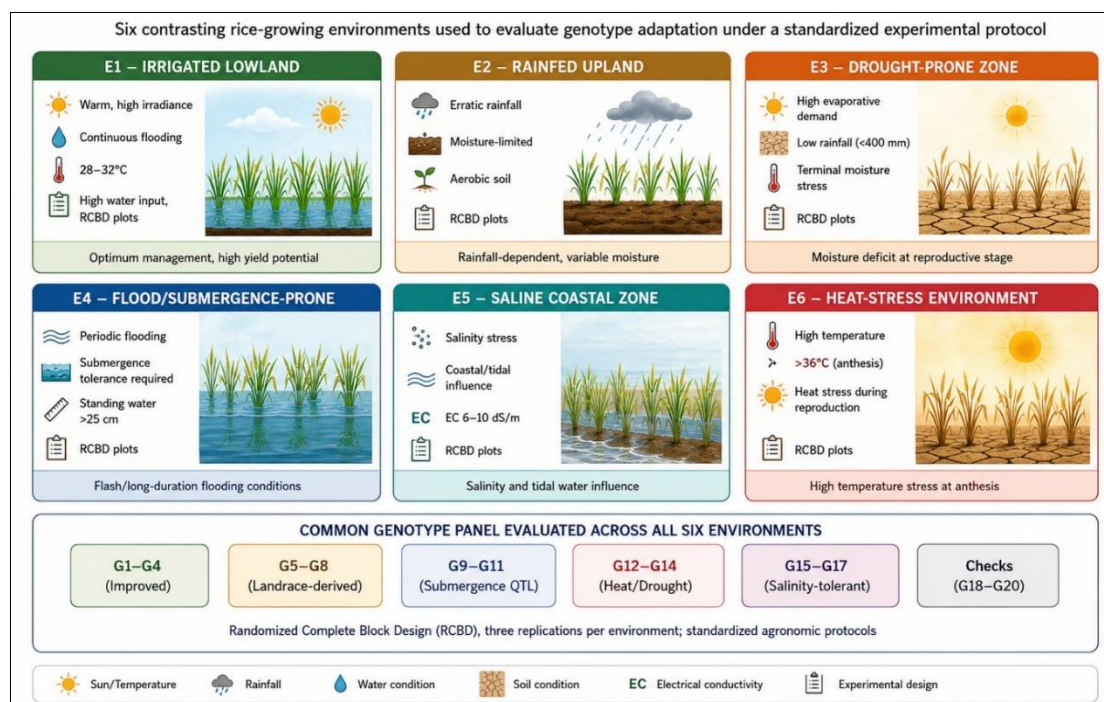


Fig 1: Schematic representation of the multi-environment trial (MET) framework, illustrating the six contrasting rice-growing environments (irrigated lowland, rainfed upland, drought-prone, flood/submergence-prone, saline coastal, and heat-stress zones) in which the common genotype panel was evaluated under a standardized experimental protocol.

Table 2: Experimental locations, climatic and edaphic conditions, and crop management practices used across the six test environments.

Code	Environment Type	Mean Temp. (°C)	Seasonal Rainfall (mm)	Soil Type / EC	Key Management Practice
E1	Irrigated lowland	28-32	850 (irrigation supplemented)	Clay loam, 0.6 dS/m	Continuous flooding, 2.5 cm ponded water
E2	Rainfed upland	26-31	620 (erratic distribution)	Sandy loam, 0.5 dS/m	Direct-seeded, no supplemental irrigation
E3	Drought-prone lowland	27-34	390 (terminal deficit)	Silty clay, 0.7 dS/m	Irrigation withheld from panicle initiation
E4	Flood/submergence-prone	26-30	1450 (monsoon peak)	Clay, 0.6 dS/m	Complete submergence 10-14 days, vegetative stage
E5	Saline coastal lowland	27-31	780	Clay loam, 6-9 dS/m	Tidal-influenced irrigation, saline groundwater
E6	Heat-stress irrigated	30-38 (anthesis window)	710 (irrigation-supplemented)	Clay loam, 0.6 dS/m	Delayed sowing to expose anthesis to peak heat

2.3. Experimental Design and Crop Management

At each of the six environments, the 20 genotypes were arranged in a Randomized Complete Block Design (RCBD) with three replications, giving a total of 360 experimental plots. Each plot consisted of six rows of 5 m length spaced 20 cm apart, with 15 cm intra-row spacing, transplanted at 21-25 days after sowing under a common regional agronomic package that included recommended fertilizer doses, need-based plant protection, and site-appropriate water management corresponding to each stress category. Border rows were excluded from data recording to minimize edge effects.

2.4. Data Recording: Agronomic, Physiological, and Yield-Related Traits

Data were recorded on days to 50% flowering, days to physiological maturity, plant height (cm), number of productive tillers per hill, panicle length (cm), number of filled grains per panicle, thousand-grain weight (g), grain yield (t/ha, adjusted to 14% moisture), biological yield (biomass, t/ha), and harvest index (%). Stress tolerance indices, including relative yield under stress relative to the irrigated control environment, were computed to complement the AMMI-based stability parameters. All observations were recorded on five randomly tagged plants per plot in addition to plot-level grain yield.

2.5. Statistical Analysis: Analysis of Variance

Data from all six environments were subjected to a combined analysis of variance (ANOVA) treating genotype, environment, and replication (nested within environment) as sources of variation, with genotype $\times$ environment interaction estimated as the residual interaction term after removing genotype and environment main effects. Homogeneity of error variances across environments was verified with Bartlett's test prior to pooling. Mean squares for genotype, environment, and $G \times E$ were tested against the pooled error mean square to assess statistical significance at $P < 0.05$ and $P < 0.01$.

2.6. AMMI Analysis and Stability Parameters

Following the combined ANOVA, the genotype $\times$ environment interaction matrix for grain yield was subjected to Additive Main Effects and Multiplicative Interaction (AMMI) analysis, in which additive genotype and environment effects were estimated by ANOVA and the multiplicative interaction structure was resolved through Principal Component Analysis (PCA) of the interaction residuals, yielding successive Interaction Principal Component Axes (IPCA1, IPCA2,...) (Zobel *et al.*, 1988; Gauch, 2006) [16, 17]. The number of significant IPCA axes retained was determined using an F-test based on Gollob's approximation. The AMMI Stability Value (ASV) was calculated as a weighted Euclidean distance

combining IPCA1 and IPCA2 scores in proportion to their explained interaction sums of squares, with lower ASV indicating greater stability (Purchase *et al.*, 2000) [18]. The Yield Stability Index (YSI) was derived by summing the rank of mean

grain yield (in descending order) and the rank of ASV (in ascending order) for each genotype, so that genotypes with low YSI combine high yield with high stability (Rao & Prabhakaran, 2005) [19].

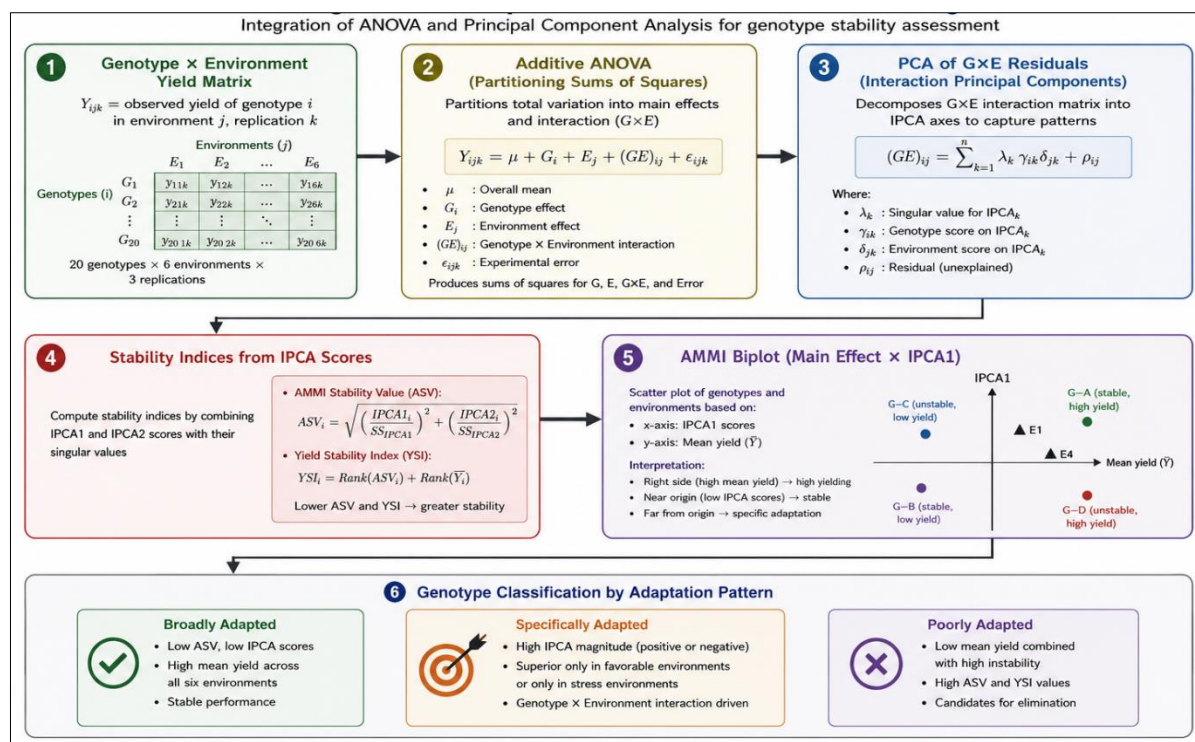


Fig 2: Conceptual framework of AMMI modeling, showing the sequential integration of additive ANOVA (partitioning genotype, environment, and G×E sums of squares), Principal Component Analysis of interaction residuals into interaction principal component axes (IPCA), derivation of the AMMI biplot, and classification of genotypes into broadly adapted, specifically adapted, and poorly adapted categories based on mean yield and stability indices.

3. Results

3.1. Mean Performance across Environments

Mean grain yield varied substantially among genotypes and environments (Table 3). Across all six environments, genotype CR-Dhan812 (G12) recorded the highest overall mean yield (5.41 t/ha), followed by CR-Dhan805 (G5, 5.20 t/ha) and CR-Dhan801 (G1, 5.03 t/ha). The irrigated lowland environment (E1) produced the highest environmental mean yield (6.07 t/ha),

while the drought-prone environment (E3) produced the lowest (3.09 t/ha), reflecting the severity of terminal moisture deficit imposed at that site. Days to flowering ranged from 78 days for the early heat-escaping genotype CR-Dhan809 (G9) to 96 days for the late-maturing landrace-derived line CR-Dhan807 (G7), while plant height ranged from 95 cm to 122 cm, with taller genotypes generally associated with submergence-tolerant backgrounds capable of elongation under partial flooding.

Table 3: Mean grain yield (t/ha) of 20 rice genotypes across six test environments (E1-E6), with overall trial mean, rank, and mean days to flowering (DF) and plant height (PH, cm).

Code	DF (d)	PH (cm)	E1	E2	E3	E4	E5	E6	Mean	Rank
G1	88	112	6.55	5.10	3.05	5.85	4.02	5.60	5.03	3
G2	90	105	6.10	5.35	3.55	4.20	3.60	5.15	4.66	9
G3	93	118	5.60	4.60	2.55	4.05	5.20	4.55	4.42	12
G4	82	98	6.40	4.80	2.95	3.90	3.55	6.05	4.61	10
G5	89	110	6.65	5.55	3.35	5.60	4.35	5.70	5.20	2
G6	87	108	6.20	5.05	3.10	5.90	3.85	5.05	4.86	5
G7	96	122	5.35	5.40	3.60	3.55	3.20	3.95	4.17	18
G8	91	115	5.75	4.30	2.60	3.65	5.35	4.10	4.29	15
G9	78	95	6.05	4.10	2.75	3.30	3.05	6.20	4.24	16
G10	86	104	6.35	5.20	3.85	4.15	3.65	5.10	4.72	8
G11	89	111	5.90	4.75	2.90	5.55	5.10	4.45	4.77	7
G12	90	113	6.70	5.75	3.65	5.80	4.60	5.95	5.41	1
G13	95	119	5.50	5.60	3.90	3.60	3.30	4.20	4.35	14
G14	85	101	6.20	4.45	2.80	3.45	3.15	6.15	4.37	13
G15	92	116	5.65	4.55	2.65	4.00	5.55	4.35	4.46	11
G16	88	109	6.30	5.30	3.40	4.90	4.10	5.85	4.97	4
G17	87	112	6.15	4.95	2.85	6.05	3.90	4.80	4.78	6
G18	89	106	6.00	4.60	2.70	4.10	3.30	4.70	4.23	17
G19	94	114	5.30	5.70	3.35	3.50	3.05	4.00	4.15	19
G20	84	100	6.75	4.20	2.30	3.10	2.80	4.60	3.96	20

3.2. Combined Analysis of Variance

The combined ANOVA (Table 4) revealed highly significant ($P < 0.01$) mean squares for environment, genotype, and genotype $\times$ environment interaction for all four traits examined in detail: grain yield, plant height, days to flowering, and harvest index. Environment accounted for the largest share of total sum of squares for grain yield (63.8%), confirming that the six test sites

imposed strongly contrasting growing conditions. Genotype (16.6%) and G $\times$ E interaction (14.5%) together accounted for a substantial additional proportion of variance, indicating that although genotypes differed consistently in their overall performance, a meaningful component of yield variation was attributable to differential genotype response across environments rather than to additive effects alone.

Table 4: Combined analysis of variance showing mean squares for genotype (G), environment (E), and genotype $\times$ environment (G $\times$ E) interaction effects for grain yield, plant height, days to flowering, and harvest index.

Source	df	MS Grain Yield (t/ha) ²	MS Plant Height (cm) ²	MS Days to Flowering (d) ²	MS Harvest Index (%) ²
Environment	5	370.00**	612.4**	182.6**	88.4**
Rep (within Env)	12	0.71	4.2	1.8	1.1
Genotype	19	25.26**	148.9**	64.3**	32.7**
G $\times$ E Interaction	95	4.42**	22.6**	9.4**	6.8**
Pooled Error	228	0.66	3.9	1.6	1.0
Total	359	-	-	-	-

** significant at $P < 0.01$. Rep = replication.

3.3. AMMI Analysis of Variance and Interaction Principal Component Axes

Partitioning of the G $\times$ E interaction sum of squares for grain yield through AMMI analysis showed that the first two interaction principal component axes (IPCA1 and IPCA2) jointly captured 79.0% of the total interaction sum of squares, with IPCA1 alone accounting for 52.0% (Table 5). Both axes were statistically significant ($P < 0.01$) by Gollob's F-test, whereas IPCA3 and the residual term, although contributing a

further 21.0% of interaction variance, were of comparatively minor magnitude and were not required for reliable stability assessment. This pattern is consistent with the AMMI2 model providing an adequate and parsimonious representation of the interaction structure for this dataset, in agreement with previous multi-environment rice trials in which the first two IPCA axes typically capture the majority of interpretable interaction pattern (Ebdon & Gauch, 2002) [20].

Table 5: AMMI analysis of variance for grain yield showing sums of squares (SS), mean squares (MS), F-values, and percentage contribution of each interaction principal component axis (IPCA) to the total genotype $\times$ environment interaction sum of squares.

Source	df	SS	MS	F	% of G $\times$ E SS
Environment	5	1850.0	370.00	562.3**	-
Genotype	19	480.0	25.26	38.4**	-
G $\times$ E Interaction	95	420.0	4.42	6.72**	100.0
IPCA1	23	218.4	9.50	14.44**	52.0
IPCA2	21	113.4	5.40	8.21**	27.0
IPCA3	19	50.4	2.65	4.03**	12.0
Residual	32	37.8	1.18	1.79 (ns)	9.0
Pooled Error	228	150.0	0.658	-	-

** significant at $P < 0.01$; ns = not significant.

3.4. Stability Parameters and Genotype Ranking

The AMMI Stability Value (ASV) ranged from 0.15 for the deep-rooted landrace-derived genotype CR-Dhan807 (G7) to 2.40 for the irrigated check BRRI dhan28 (G20), while the Yield Stability Index (YSI), which jointly considers yield rank and ASV rank, identified CR-Dhan812 (G12), CR-Dhan810 (G10), and CR-Dhan816 (G16) as the genotypes combining the most

favorable balance of high yield and low interaction variance (Table 6, Figure 2). By contrast, genotypes such as BRRI dhan28 (G20) and the heat-tolerant lines CR-Dhan809 (G9) and CR-Dhan814 (G14) displayed comparatively high ASV values despite reasonable mean yield in specific environments, reflecting pronounced crossover interaction and specific rather than broad adaptation.

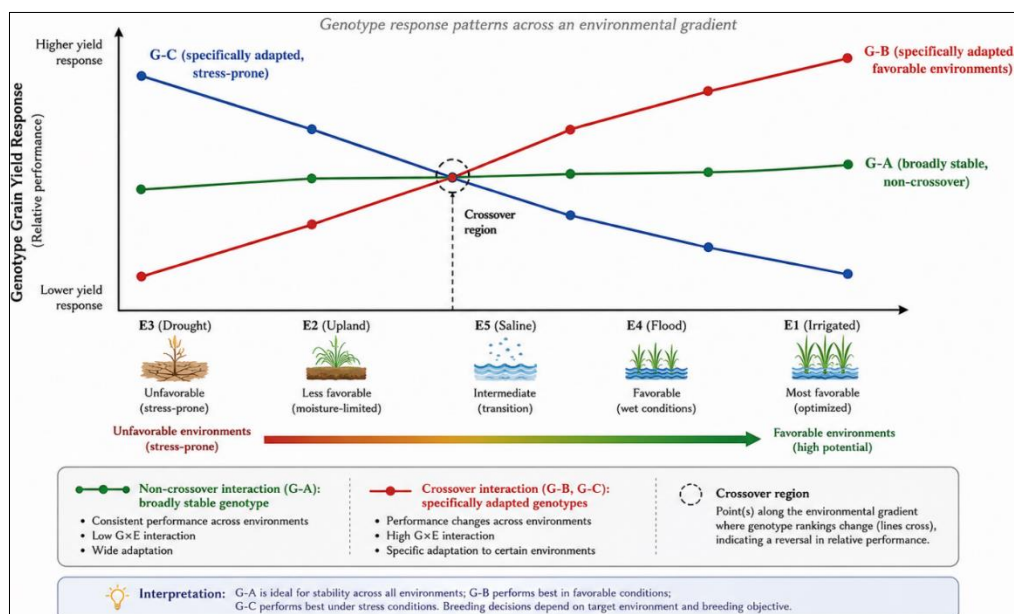


Fig 3: Conceptual schematic of genotype × environment interaction illustrating a broadly stable, non-crossover genotype response (G-A) and two specifically adapted, crossover-type genotype responses (G-B favoring favorable environments; G-C favoring stress-prone environments) across an environmental gradient from unfavorable to favorable conditions, with the crossover region indicating where genotype rankings reverse.

Table 6: Comparative ranking of rice genotypes based on grain yield, AMMI stability value (ASV), yield stability index (YSI), stress tolerance category, and inferred breeding potential.

Code	Yield Rank	ASV	ASV Rank	YSI	YSI Rank	Adaptation Pattern	Breeding Potential
G12	1	0.61	8	9	1	Broadly adapted	High
G10	8	0.37	3	11	2	Broadly adapted	High
G16	4	0.58	7	11	3	Broadly adapted	High
G11	7	0.49	5	12	4	Broadly adapted	High
G5	2	0.85	13	15	5	Broadly adapted	High
G2	9	0.41	4	13	6	Broadly adapted	Moderate-High
G13	14	0.21	2	16	7	Specifically adapted (drought)	Moderate
G3	12	0.51	6	18	8	Specifically adapted (saline)	Moderate
G6	5	0.93	14	19	9	Specifically adapted (E4)	Moderate-High
G1	3	1.26	16	19	9	Specifically adapted (E4)	Moderate-High
G7	18	0.15	1	19	9	Specifically adapted (drought)	Low-Moderate
G15	11	0.65	10	21	12	Specifically adapted (saline)	Moderate
G17	6	1.20	15	21	12	Specifically adapted (E4)	Moderate
G8	15	0.78	11	26	14	Specifically adapted (saline)	Low-Moderate
G18	17	0.83	12	29	17	Poorly adapted	Low
G19	19	0.62	9	28	16	Poorly adapted	Low
G4	10	1.63	17	27	15	Specifically adapted (heat)	Moderate
G14	13	2.01	18	31	18	Specifically adapted (heat)	Low-Moderate
G9	16	2.09	19	35	19	Specifically adapted (heat)	Low
G20	20	2.40	20	40	20	Poorly adapted	Low

4. Discussion

4.1. Genotype Performance and Environmental Influence

The overwhelming contribution of environment to total variance in this study (63.8% for grain yield) is consistent with the general finding across multi-environment rice trials that site-to-site differences in water availability, temperature, and soil salinity typically exceed genetic differences among tested genotypes (Sabaghnia *et al.*, 2008; Verma *et al.*, 2020) [21, 22]. This underscores the risk of extrapolating single-location results to broader recommendation domains and reinforces the necessity of the multi-environment design and interaction analysis applied here. The substantial G×E interaction sum of squares (14.5% of total, and statistically significant at $P < 0.01$) further confirms that genotype ranking was not uniform across the six environments, necessitating explicit stability analysis rather than reliance on mean performance alone.

4.2. Distinguishing Stable from High-Yielding Genotypes

A central finding of the AMMI analysis was the clear separation between genotypes combining high mean yield with low ASV (broadly adapted, e.g., G12, G10, G16, G11) and genotypes exhibiting pronounced crossover interaction, performing well only in specific environments (e.g., G1 and G6 in the submergence-prone environment E4; G9 and G14 under heat stress at E6). This pattern exemplifies the classical distinction between non-crossover and crossover G×E interaction described in foundational stability literature (Mekbib, 2003) [23], and demonstrates the practical value of jointly considering yield rank and stability rank through the YSI, since selection on mean yield alone would have favored several genotypes whose apparent superiority was later shown to be environment-specific rather than genuinely superior in a general sense.

4.3. Comparison with Previous G×E and AMMI Studies in Rice

The proportion of interaction sum of squares captured by the first two IPCA axes in this study (79.0%) falls within the range commonly reported in AMMI-based rice multi-environment trials, where the first two axes typically explain between 65% and 85% of interaction variance, supporting the adequacy of an AMMI2-type model for stability interpretation in comparable datasets (Ahmadi *et al.*, 2015; Kaya *et al.*, 2006) ^[24, 25]. However, some previous studies conducted across a narrower range of environmental contrasts have reported lower G×E magnitude relative to genotype main effects, suggesting that the inclusion of strongly divergent stress environments, as adopted in the present six-environment design, tends to amplify detectable interaction relative to trials confined to more homogeneous production zones (Dixit *et al.*, 2017) ^[26]. This comparison highlights those that environmental range, and not merely genotype number, is a key determinant of the interaction magnitude observed in any given MET.

4.4. Breeding and Varietal Recommendation Implications

From a practical breeding standpoint, genotypes identified as broadly adapted with low YSI, particularly CR-Dhan812 and CR-Dhan810, represent strong candidates for wide-scale varietal release across multiple production ecologies, while genotypes exhibiting strong specific adaptation, such as CR-Dhan801 and CR-Dhan806 for submergence-prone lowlands or CR-Dhan803 and CR-Dhan815 for saline coastal zones, can be strategically targeted for release within their specific recommendation domains rather than discarded on the basis of moderate overall mean yield (Singh *et al.*, 2010) ^[27]. This dual strategy, combining broad-adaptation cultivars for large mega-environments with niche-adapted cultivars for narrowly defined stress zones, mirrors current best practice in climate-resilient variety deployment programs.

4.5. Methodological Strengths and Limitations

The principal strength of the AMMI approach applied here lies in its capacity to separate genuine interaction pattern from experimental noise through PCA decomposition, generating interpretable, low-dimensional stability statistics (ASV, YSI) that can be readily communicated to breeding decision-makers. Nonetheless, AMMI remains a fixed-effects, single-trait framework that does not directly model environmental covariates, meaning that the biological drivers of interaction (e.g., specific temperature or salinity thresholds) must be inferred post hoc from environmental characterization rather than estimated within the model itself. Complementary approaches such as factorial regression, Finlay-wilkinson joint regression, or environmental covariate-based genomic prediction models could further resolve the specific environmental drivers underlying the interaction patterns identified in this study, and represent a natural extension of the present analysis.

5. Climate Adaptation and Rice Improvement

5.1. Climate-Smart Breeding Strategies

Climate-smart rice breeding integrates stress tolerance, resource-use efficiency, and yield stability as co-equal breeding objectives alongside conventional yield potential, recognizing that future production environments will increasingly deviate from the historically stable conditions under which many current mega-varieties were developed. Multi-environment evaluation frameworks of the type applied in this study provide the empirical foundation for such breeding strategies by directly

quantifying which combinations of tolerance traits translate into measurable yield stability under realistic field conditions rather than controlled stress-screening alone.

5.2. Variety Recommendation and Farmer Adoption

Effective translation of stability analysis into farmer benefit requires that recommendation domains be clearly communicated, distinguishing genotypes suited to broad release from those suited to specific agro-ecological niches. Farmer adoption of climate-resilient cultivars is strongly influenced by perceived yield stability across seasons rather than by maximum yield potential under a single favorable season, making stability statistics such as those generated here directly relevant to extension messaging and seed system planning in climate-vulnerable regions.

5.3. Food Security and Sustainable Rice Production

Because rice remains the dominant calorie source for a large proportion of the global population, yield instability at the level of individual farms aggregates into systemic food security risk at regional and national scales. Deploying genotypes with demonstrated cross-environment stability, particularly in regions subject to recurrent drought, flooding, or salinity, contributes directly to buffering national production against the increasing climatic variability projected under most future emission scenarios, while also supporting more sustainable input use where stable genotypes reduce the need for compensatory fertilizer or irrigation applications under variable conditions.

5.4. Integration with Precision Breeding Pipelines

The genotype classification generated through AMMI and stability analysis in this study can be directly integrated into precision breeding pipelines by prioritizing broadly adapted, high-YSI genotypes as recurrent parents in subsequent crossing cycles, while retaining specifically adapted genotypes as targeted donors for their respective stress-tolerance mechanisms. This integration allows breeding programs to simultaneously pursue genetic gain in mean performance and improvement in stability, rather than treating these as competing or sequential objectives.

6. Emerging Technologies and Future Perspectives

6.1. High-Throughput Phenotyping and Remote Sensing

High-throughput phenotyping platforms employing unmanned aerial vehicles, multispectral and thermal imaging, and ground-based sensor networks now enable rapid, non-destructive characterization of canopy temperature, vegetation indices, and biomass accumulation across large multi-environment trial networks, substantially increasing the density and precision of environmental characterization relative to the manual approaches used in the present study. Integration of such phenotyping data with AMMI-type stability models offers the prospect of directly linking physiological stress responses to interaction pattern rather than inferring these relationships indirectly.

6.2. Genomics, GWAS, and Genomic Selection

Genome-wide association studies (GWAS) conducted across genotype panels evaluated in multi-environment trials increasingly allow interaction effects themselves to be mapped to specific genomic regions, distinguishing loci with stable effects across environments from those exhibiting genotype-by-environment-specific expression. Genomic selection models incorporating environmental covariates further extend this capacity by predicting genotype performance in untested

environments, potentially reducing the number of physical testing sites required in future MET networks while maintaining or improving prediction accuracy for both mean performance and stability.

6.3. Artificial Intelligence and Machine Learning in Breeding

Machine learning approaches, including random forests, gradient boosting, and deep neural networks, are increasingly applied to multi-environment trial data to model complex, non-linear G×E relationships that may not be fully captured by the bilinear structure of the AMMI model. Such approaches, when combined with environmental covariate data and historical trial archives, hold promise for predicting genotype performance and stability in novel or future climate scenarios that fall outside the range of conditions directly sampled by current test environments.

6.4. Multi-Location Breeding Networks and Future Research Priorities

Expanding coordinated multi-location breeding networks, in which common genotype panels are systematically evaluated across an expanding range of climatically representative sites, will be essential for capturing the full spectrum of environmental variability relevant to future climate scenarios. Future research priorities include the integration of environmental covariate modeling with AMMI and genomic prediction frameworks, the development of dynamic stability indices capable of incorporating within-season environmental fluctuation, and the systematic incorporation of farmer-participatory evaluation to validate stability rankings under real production conditions beyond the research station environments used in formal MET analysis.

7. Conclusion

In this study, the effects of 20 varieties of rice grown in six completely different areas were studied, and it was found that together the effects of the environment and the genotype and environment interaction made a large contribution to the total variations of the final yields of the rice. Thus, the importance of testing varieties in several locations was demonstrated as being necessary for correct variety recommendation. AMMI modeling approach makes it possible to separate the interaction structure by taking into account the first two axes, which covered most of the interaction variance. It was also possible to group cultivars according to their adaptation criteria. CR-Dhan812, CR-Dhan810, and CR-Dhan816 proved to be the best choices due to their high average yield and little interaction variance, while several other cultivars, which can be resistant to one type of stress only, may be used in certain regions. It has been shown how effective AMMI-based stability assessment combined with classical quantitative genetic analysis can be in selecting climate-resilient rice through dual strategy of broad-adaptation mega-varieties and stress adapted cultivars. In the future, it is planned to implement the use of high-throughput phenotyping for climatic predictions and machine learning-based modeling for interaction assessments to create rice varieties faster and with higher resilience.

References

1. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology*. 2005;59(1):1-6.
2. Mohanty S, Wassmann R, Nelson A, Moya P, Jagadish SVK. Rice and climate change: significance for food security and vulnerability. *IRRI Discussion Paper Series*. 2013;49:1-14.
3. Wassmann R, Jagadish SVK, Heuer S, Ismail A, Redona E, Serraj R, *et al.* Climate change affecting rice production: the physiological and agronomic basis for possible adaptation strategies. *Advances in Agronomy*. 2009;101:59-122.
4. Zhao C, Liu B, Piao S, Wang X, Lobell DB, Huang Y, *et al.* Temperature increase reduces global yields of major crops in four independent estimates. *Proceedings of the National Academy of Sciences of the United States of America*. 2017;114(35):9326-9331.
5. Sarkar RK, Reddy JN, Sharma SG, Ismail AM. Physiological basis of submergence tolerance in rice and implications for crop improvement. *Current Science*. 2006;91(7):899-906.
6. Jagadish SVK, Craufurd PQ, Wheeler TR. High temperature stress and spikelet fertility in rice (*Oryza sativa* L.). *Journal of Experimental Botany*. 2007;58(7):1627-1635.
7. Ismail AM, Horie T. Genomics, physiology, and molecular breeding approaches for improving salt tolerance. *Annual Review of Plant Biology*. 2017;68:405-434.
8. Atlin GN, Cairns JE, Das B. Rapid breeding and varietal replacement are critical to adaptation of cropping systems in the developing world to climate change. *Global Food Security*. 2017;12:31-37.
9. Collard BCY, Mackill DJ. Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philosophical Transactions of the Royal Society B: Biological Sciences*. 2008;363(1491):557-572.
10. Crossa J, Perez-Rodriguez P, Cuevas J, Montesinos-Lopez O, Jarquin D, de los Campos G, *et al.* Genomic selection in plant breeding: methods, models, and perspectives. *Trends in Plant Science*. 2017;22(11):961-975.
11. Xu K, Xu X, Fukao T, Canlas P, Maghirang-Rodriguez R, Heuer S, *et al.* Sub1A is an ethylene-response-factor-like gene that confers submergence tolerance to rice. *Nature*. 2006;442(7103):705-708.
12. Kumar A, Dixit S, Ram T, Yadaw RB, Mishra KK, Mandal NP. Breeding high-yielding drought-tolerant rice: genetic variations and conventional and molecular approaches. *Journal of Experimental Botany*. 2014;65(21):6265-6278.
13. Yan W, Kang MS. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. Boca Raton: CRC Press; 2003.
14. Eberhart SA, Russell WA. Stability parameters for comparing varieties. *Crop Science*. 1966;6(1):36-40.
15. Annicchiarico P. Genotype × Environment Interactions: Challenges and Opportunities for Plant Breeding and Cultivar Recommendations. Rome: Food and Agriculture Organization of the United Nations; 2002. p.1-115.
16. Zobel RW, Wright MJ, Gauch HG. Statistical analysis of a yield trial. *Agronomy Journal*. 1988;80(3):388-393.
17. Gauch HG. Statistical analysis of yield trials by AMMI and GGE. *Crop Science*. 2006;46(4):1488-1500.
18. Purchase JL, Hatting H, van Deventer CS. Genotype × environment interaction of winter wheat in South Africa: II. Stability analysis of yield performance. *South African Journal of Plant and Soil*. 2000;17(3):101-107.
19. Rao AR, Prabhakaran VT. Use of AMMI in simultaneous selection of genotypes for yield and stability. *Journal of the Indian Society of Agricultural Statistics*. 2005;59(1):76-82.
20. Ebdon JS, Gauch HG. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype ×

- environment interaction. *Crop Science*. 2002;42(2):489-496.
21. Sabaghnia N, Dehghani H, Sabaghpour SH. Graphic analysis of genotype $\times$ environment interaction for lentil yield in Iran. *Agronomy Journal*. 2008;100(3):760-764.
 22. Verma A, Kumar N, Kharab AS, Sharma A. GGE biplot and AMMI analysis of yield stability in multi-environment wheat trials. *Field Crops Research*. 2020;255:107866.
 23. Mekbib F. Yield stability in common bean (*Phaseolus vulgaris* L.) genotypes. *Euphytica*. 2003;130(2):147-153.
 24. Ahmadi J, Vaezi B, Shaabani A, Khademi K, Fabriki-Ourang S, Pour-Aboughadareh A. Genotype-environment interaction and stability analysis for grain yield in some barley genotypes. *Revista de la Facultad de Ciencias Agrarias*. 2015;47(2):125-136.
 25. Kaya Y, Akcura M, Taner S. GGE-biplot analysis of multi-environment yield trials in bread wheat. *Turkish Journal of Agriculture and Forestry*. 2006;30(5):325-337.
 26. Dixit S, Singh A, Sandhu N, Bhandari A, Vikram P, Kumar A. Combining drought and submergence tolerance in rice: marker-assisted breeding and QTL combination effects. *Molecular Breeding*. 2017;37(12):143.
 27. Singh RK, Redona E, Refuerzo L. Varietal improvement for abiotic stress tolerance in rice: progress and prospects. In: Pareek A, Sopory SK, Bohnert HJ, Govindjee, editors. *Abiotic Stress Adaptation in Plants*. Dordrecht: Springer; 2010. p.133-147.